

FIG. 1.

1 GGGAGTCATCATM S D V T I V K E G W V Q K R G E 17  
 61 ATATATAAAAACTGGAGGCCAAGATACTTCCTTTTGAAAGACAGATGGCTCATTCATAGG 37  
 121 ATATAAAGAGAAAACCTCAAGATGTGGATTTACCTTATCCCTCAACAACCTTTTCAGTGGC 57  
 181 AAAATGCCAGTTAATGAAAACAGAACGACCAAAGCCAAACACATTTATAATCAGATGTCT 77  
 241 CCAGTGGACTACTGTTATAGAGAGAACATTTTCATGTAGATACTCCAGAGGAAAGGGAAGA 97  
 301 ATGGACAGAAGCTATCCAGGCTGTAGCAGACAGACTGCAGAGGCAAGAAGAGGAGAGAAT 117  
 361 GAATTGTAGTCCAACCTTCACAAATTGATAATATAGGAGAGGAAGAGATGGATGCCTCTAC 137  
 421 AACCCATCATAAAAGAAAGACAATGAATGATTTTGACTATTTGAAACTACTAGGTAAAGG 157  
 481 CACTTTTGGGAAAGTTATTTTGGTTTCGAGAGAAGGCAAGTGAAAATACTATGCTATGAA 177  
 541 GATTCTGAAGAAAGAAGTCATTATTGCAAAGGATGAAGTGGCACACACTCTAACTGAAAG 197  
 601 CAGAGTATTAAAGAACACTAGACATCCCTTTTTTAACATCCTTGAAATATTCCTTCCAGAC 217  
 661 AAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTCCATTT 237  
 721 GTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTGTCTC 257  
 781 TGCCTTGGACTATCTACATTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGGAGAATCT 277  
 841 AATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAGAAGGGAT 297  
 901 CACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCAGAGGT 317  
 961 GTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGGTTGTCATGTA 337  
 1021 TGAAATGATGTGTGGGAGGTTACCTTTCTACAACCAGGACCATGAGAACTTTTTGAATT 357  
 1081 AATATTAATGGAAGACATTAAATTTCTCAGAACTCTCTTCAGATGCAAAATCATTGCT 377  
 1141 TTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACCAGATGATGCAAA 397  
 1201 AGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAA 417  
 1261 GCTTGTACCTCCTTTTAACTCTCAAGTAACATCTGAGACAGATACTAGATATTTTGATGA 437  
 1321 AGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGATGGTAT 457  
 1381 GGACTGCATGGACAATGAGAGCGCGCCGCAATTTCCCTCAATTTTCTACTCTGCAAGTGG 477  
 1441 ACGAGAATAAGTCTCTTTCAATTCTGCTACTTCACTGTCACTCTTCAATTTATTACTGAAAA 479  
 1501 TGATTCTCTGGACATCACCAGTCCTAGCTCTTACACATAGCAGGGGCA

FIG. 2.

Akt-1 : MVTVAKEGWAIRGEYIKWRPRYELIKNDGTFIGYKEPDDVDLPEALNNFSVAQCQLMKTERPFPNTFIRCLQWITVIERTFHV : 90  
 Akt-2 : MVEUSVIKEGWAIRGEYIKWRPRYELIKSDGTFIGYKEPDDVDLPEALNNFSVAQCQLMKTERPFPNTFIRCLQWITVIERTFHV : 90  
 Akt-3 : MVTVAKEGWAIRGEYIKWRPRYELIKNDGTFIGYKEPDDVDLP-YELNNFSVAKCQLMKTERPFPNTFIRCLQWITVIERTFHV : 89

Akt-1 : EEPEREERWTAIQVAGLKKOE--EPPDRS--SSSDISAEEMBSLAKQZHRVIMNIEFEVLKLLGKGTGKVVILVKEKAGHYVAM : 178  
 Akt-2 : DSPDEREERWTAIQVANSIQRAPGEDPMYKCS--SDSETTEEMAVAVSARAKVIMNIEFEVLKLLGKGTGKVVILVKEKAGHYVAM : 180  
 Akt-3 : DTPEREERWTAIQVAGLQLOQE--EPPMCSPTSOIDNIEEEDDAS--THH--EKTMMNIEFEVLKLLGKGTGKVVILVKEKAGHYVAM : 176

Akt-1 : KILLKEVIKAKDEVANTITEERVLKNSRHPFLTILKYSFQIDRLCFVMEYVNGGELFFHLSRERVFEEDRREYGAIEVSALYLLHSEK : 268  
 Akt-2 : KILLKEVIKAKDEVANTITEERVLKNSRHPFLTILKYSFQIDRLCFVMEYVNGGELFFHLSRERVFEEDRREYGAIEVSALYLLHS-R : 269  
 Akt-3 : KILLKEVIKAKDEVANTITEERVLKNSRHPFLTILKYSFQIDRLCFVMEYVNGGELFFHLSRERVFEEDRREYGAIEVSALYLLHS-G : 265

Akt-1 : KIVYRDVKLENMLDKDGHKIKITDFGLCKEGIKD--ATMKTFCGTPPEYLAPVLELDNDYGRAVDWVGLGVVMYEMCGRLPFYHQDHEKLF : 358  
 Akt-2 : DVYRDVKLENMLDKDGHKIKITDFGLCKEGISD--ATMKTFCGTPPEYLAPVLELDNDYGRAVDWVGLGVVMYEMCGRLPFYHQDHEKLF : 359  
 Akt-3 : KIVYRDVKLENMLDKDGHKIKITDFGLCKEGITD--ATMKTFCGTPPEYLAPVLELDNDYGRAVDWVGLGVVMYEMCGRLPFYHQDHEKLF : 355

Akt-1 : ELIINEIIFPRTLSDAKSLLSGILLKQDPQRLGGGSSDAKEEIOHNFAGITWQWVFEKKLSPPFKPOVTSEIDTRYFDEFTAQMIT : 448  
 Akt-2 : ELIINEIIFPRTLSDAKSLLSGILLKQDPQRLGGGSSDAKEVMEHNFELSILWQWVQKLLPPFKPOVTSEIDTRYFDEFTAQMIT : 449  
 Akt-3 : ELIINEDIKFRTLSDAKSLLSGILLKQDPNKRLLGGGDDAKEEIOHNFAGITWQWVFEKKLSPPFKPOVTSEIDTRYFDEFTAQMIT : 445

Akt-1 : ITPPDODD--E--EVSSEERMEPQFSYSASATA : 480  
 Akt-2 : ITPPDODD--E--EVSSEERMEPQFSYSASATA : 481  
 Akt-3 : ITPPEKDEDD--E--EVSSEERMEPQFSYSASATA : 479

FIG. 3.

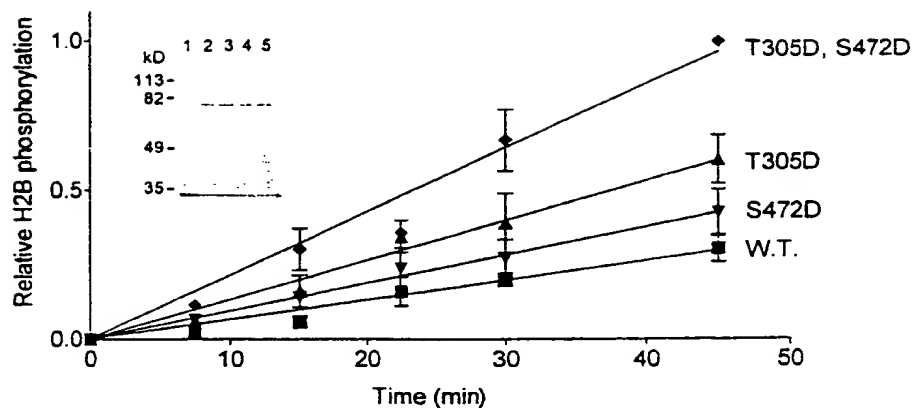
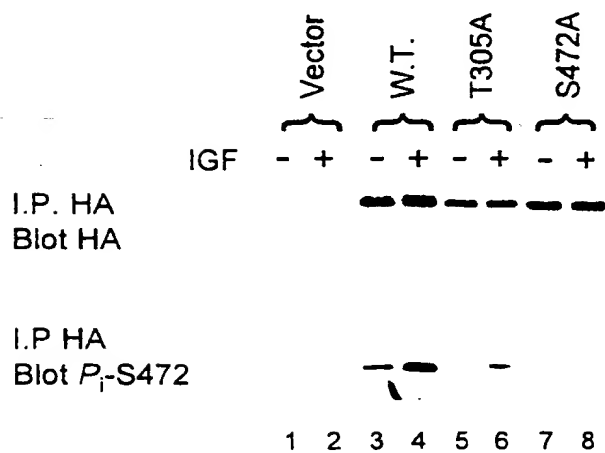
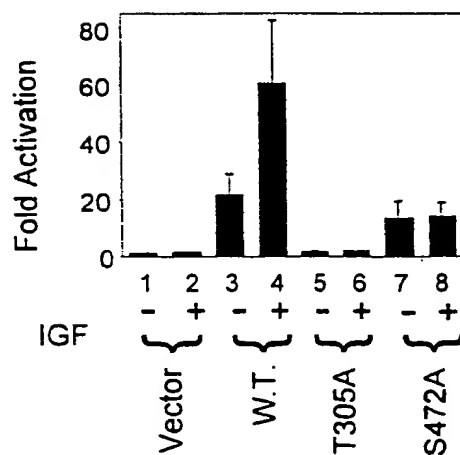
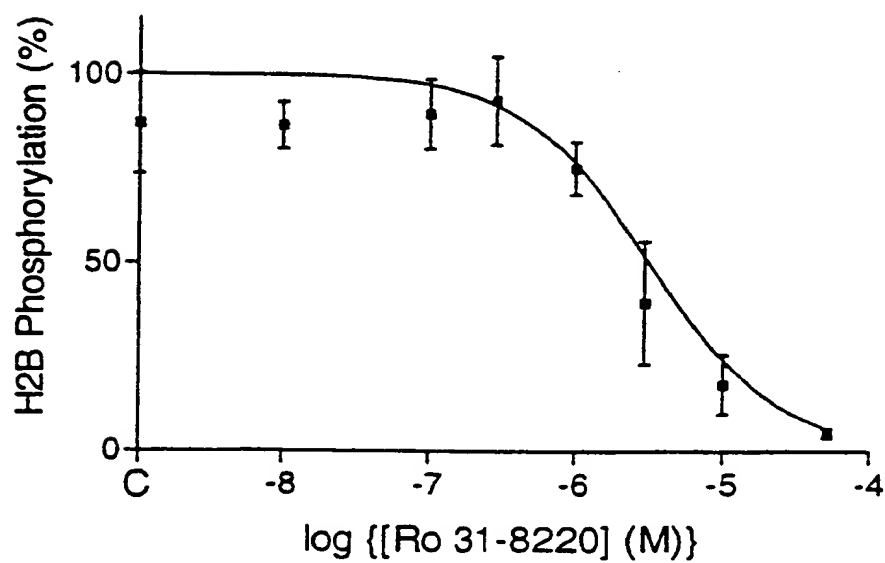
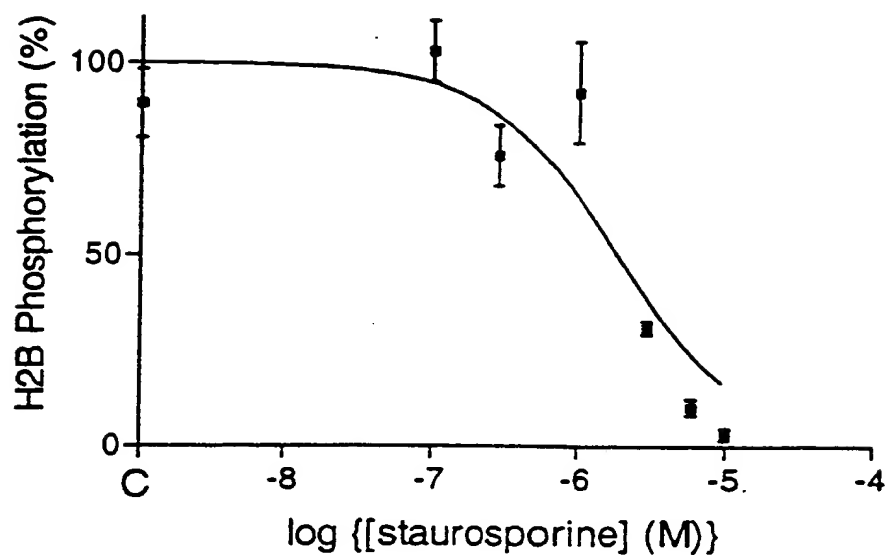
**A****B****C**

FIG. 4.



*FIG. 5.*

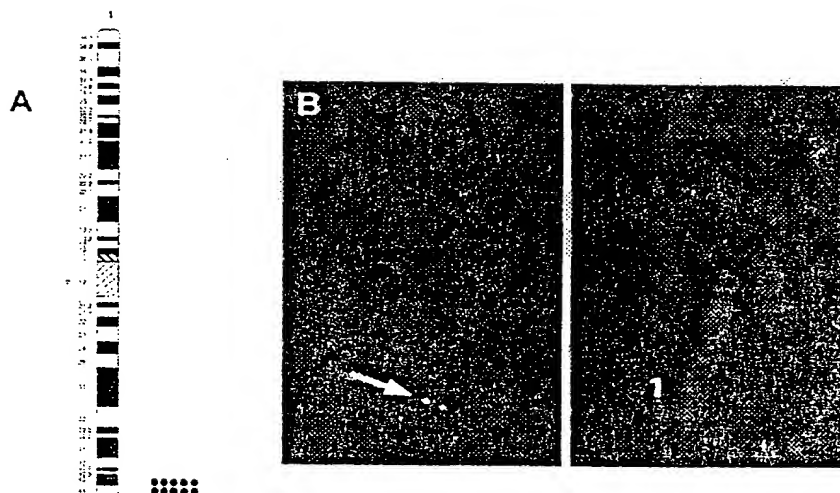


FIG. 6A.

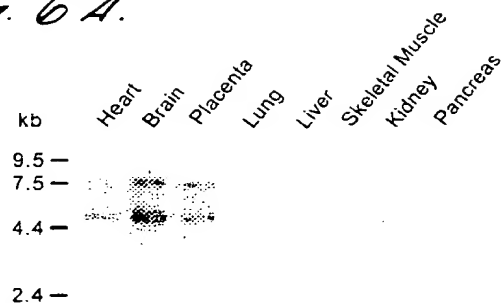


FIG. 6B.

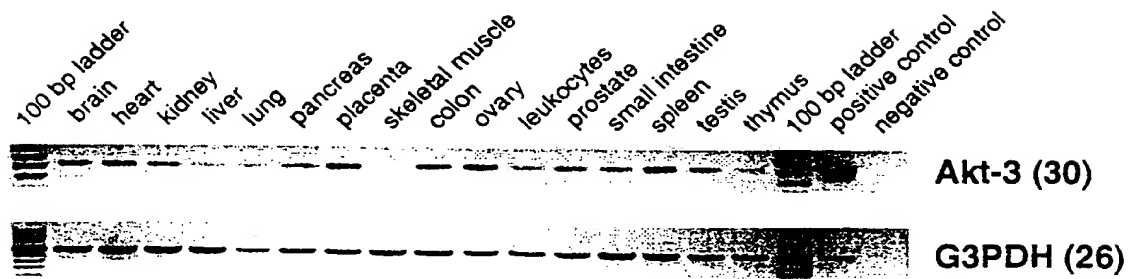
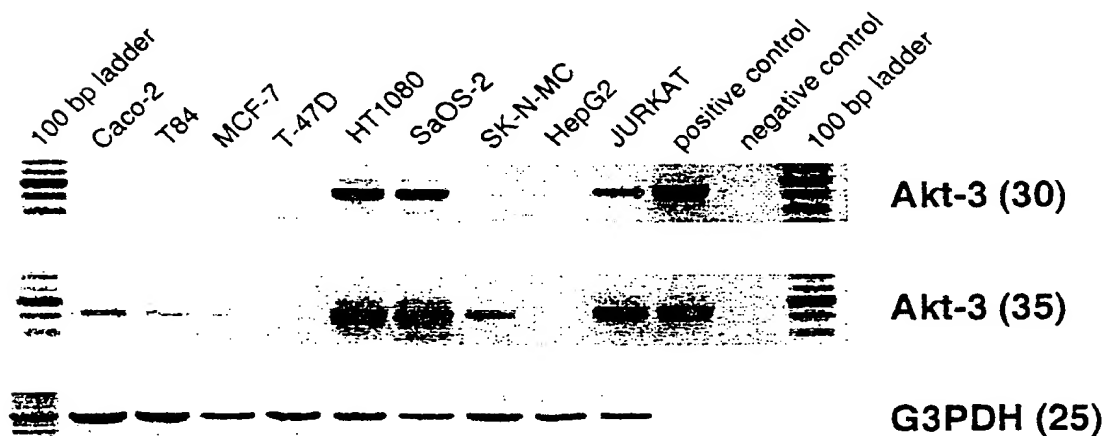
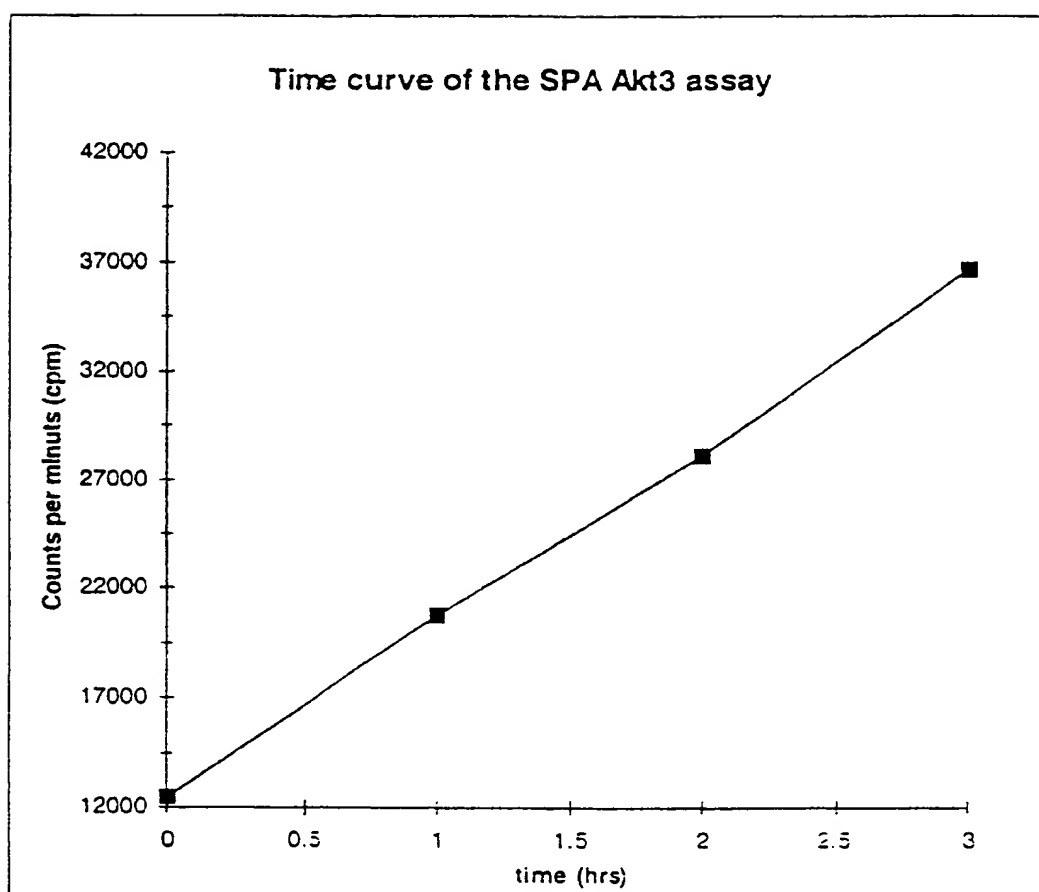


FIG. 6C.



*FIG. 7.*

*FIG. 8.*